

Run on: July 6, 2004, 13:57:03 ; Search time 52.508 Seconds  
 (without alignments)  
 1382.059 Million cell updates/sec

Title: US-10-063-588-80  
 Perfect score: 1174  
 Sequence: 1 MASLGLQLVGYYILGLLGLLG.....PGQPPKVKSEFNSSLTGYV 230

Scoring table: BLOSUM62  
 Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0  
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
 Maximum Match 100%  
 Listing first 45 summaries

Database : SPTREMBL\_25:\*  
 1: sp\_archaea:\*  
 2: sp\_bacteria:\*  
 3: sp\_fungi:\*  
 4: sp\_human:\*  
 5: sp\_invertebrate:\*  
 6: sp\_mammal:\*  
 7: sp\_mhc:\*  
 8: sp\_organelle:\*  
 9: sp\_phage:\*  
 10: sp\_plant:\*  
 11: sp\_rodent:\*  
 12: sp\_virus:\*  
 13: sp Vertebrate:\*  
 14: sp\_unclassified:\*  
 15: sp\_rvirus:\*  
 16: sp\_bacteriap:\*  
 17: sp\_archeap:\*

# SUMMARIES

Result No.	Score	% Query		Length	DB	ID	Description
		Match					
1	456	38.8		218	13	Q90XR2	Q90xr2 brachydanio
2	452	38.5		213	13	Q7ZSZ2	Q7zsz2 xenopus lae
3	448.5	38.2		219	11	Q810I9	Q810i9 mus musculu
4	448	38.2		213	13	Q805G0	Q805g0 xenopus lae
5	446	38.0		215	13	Q90XR8	Q90xr8 brachydanio
6	444.5	37.9		209	13	Q90XR9	Q90xr9 brachydanio
7	438	37.3		210	13	Q90XQ8	Q90xq8 brachydanio
8	432.5	36.8		214	13	Q90XQ9	Q90xq9 xenopus lae
9	430	36.6		214	13	Q9DE12	Q9de12 xenopus lae
10	428.5	36.5		214	13	Q98SR2	Q98sr2 gallus gall
11	421	35.9		214	13	Q90XR0	Q90xr0 brachydanio

12	419	35.7	214	13	Q7T2P4	Q7t2p4 brachydanio
13	417.5	35.6	210	13	Q90XR4	Q90xr4 brachydanio
14	413.5	35.2	206	13	Q90XS1	Q90xs1 brachydanio
15	399.5	34.0	211	4	Q7Z4X9	Q7z4x9 homo sapien
16	396	33.7	211			

Run on: July 6, 2004, 13:58:13 ; Search time 19.9678 Seconds  
 (without alignments)  
 1107.984 Million cell updates/sec

Title: US-10-063-588-80  
 Perfect score: 1174  
 Sequence: 1 MASLGLQLVGYILGLLGLLG.....PGQPPKVKSEFNLSYSLTGYV 230

Scoring table: BLOSUM62  
 Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0  
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
 Maximum Match 100%  
 Listing first 45 summaries

Database : PIR\_78:\*  
 1: pir1:\*  
 2: pir2:\*  
 3: pir3:\*  
 4: pir4:\*

# SUMMARIES

Result No.	Score	Query		DB	ID	Description
		Match	Length			
1	423.5	36.1	280	2	A39484	androgen-withdrawa
2	100	8.5	400	2	AG2866	MFS permease [drug
3	100	8.5	400	2	D97643	probable efflux pr
4	99.5	8.5	330	2	C69648	2-keto-3-deoxygluc
5	99.5	8.5	463	2	F90285	metabolite transpo
6	97.5	8.3	484	2	C75609	amino acid ABC tra
7	95.5	8.1	458	2	H71657	NADH2 dehydrogenas
8	93	7.9	523	2	T11916	NADH2 dehydrogenas
9	91	7.8	160	2	JN0503	peripheral myelin
10	90.5	7.7	487	2	T19237	hypothetical prote
11	90.5	7.7	617	2	F71019	hypothetical prote
12	88.5	7.5	429	2	A97241	permease [imported
13	88.5	7.5	521	2	A99549	amino acid permeas
14	88.5	7.5	593	2	H71283	conserved hypothet
15	88	7.5	160	2	A41144	growth arrest-rela

Run on: July 6, 2004, 13:56:23 ; Search time 14.791 Seconds  
(without alignments)  
809.691 Million cell updates/sec

Title: US-10-063-588-80  
Perfect score: 1174  
Sequence: 1 MASLGLQLVGYYILGLLGLLG.....PGQPPKVKSEFNSYSLTGYV 230

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : SwissProt\_42:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result		%					
No.	Score	Match	Length	DB	ID	Description	
1	1174	100.0	230	1	CLD2_HUMAN	P57739	homo sapien
2	1119	95.3	230	1	CLD2_CANFA	Q95km6	canis famil
3	1096	93.4	230	1	CLD2_MOUSE	O88552	mus musculu
4	571	48.6	239	1	CLDE_HUMAN	O95500	homo sapien
5	561.5	47.8	239	1	CLDE_MOUSE	Q9z0s3	mus musculu
6	459.5	39.1	208	1	CLDY_BRARE	Q9yh91	brachydanio
7	450.5	38.4	218	1	CLD3_CANFA	Q95km5	canis famil
8	450	38.3	220	1	CLD3_HUMAN	O15551	homo sapien
9	446	38.0	210	1	CLD4_MOUSE	O35054	mus musculu
10	443.5	37.8	209	1	CLD4_CERAE	O19005	cercopithec

XX  
 PS Claim 1; Page 12 (Disclosure); 42pp; Chinese.  
 XX  
 CC The present sequence represents human SP82 protein, which has cancer-  
 CC suppressing activity. The present invention also describes a method for  
 CC the preparation of the protein by recombination, and the application of  
 CC the protein in treating diseases such as cancer  
 XX  
 SQ Sequence 230 AA;

Query Match 100.0%; Score 1174; DB 5; Length 230;  
 Best Local Similarity 100.0%; Pred. No. 7.3e-117;  
 Matches 230; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MASLGLQLVGYYILGLLGLLSTLVAMLLPSWKTSSYVQASIVTAVGFSGKLWMECATHSTG 60  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 1 MASLGLQLVGYYILGLLGLLSTLVAMLLPSWKTSSYVQASIVTAVGFSGKLWMECATHSTG 60  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Qy 61 ITQCDIYSTLLGLPADIQAAQAMMVTSSAIISSLACIISVVGMRCTVFCQESRAKDRVAVA 120  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 61 ITQCDIYSTLLGLPADIQAAQAMMVTSSAIISSLACIISVVGMRCTVFCQESRAKDRVAVA 120  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Qy 121 GGVFIFILGGLLGFIPVAVNLHGIILRDFYSPLVPDSMKFGEALYLGIISSLFSLIAGII 180  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 121 GGVFIFILGGLLGFIPVAVNLHGIILRDFYSPLVPDSMKFGEALYLGIISSLFSLIAGII 180  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Qy 181 LCFSCSSQNRNSNYDAYQAQPLATRSSPRPGQPPKVKSEFNSSYSLTGYV 230  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 181 LCFSCSSQNRNSNYDAYQAQPLATRSSPRPGQPPKVKSEFNSSYSLTGYV 230  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Search completed: July 6, 2004, 14:00:34  
 Job time : 76.2154 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: July 6, 2004, 13:58:48 ; Search time 63.6013 Seconds  
 (without alignments)  
 1125.689 Million cell updates/sec

Title: US-10-063-588-80  
 Perfect score: 1174  
 Sequence: 1 MASLGLQLVGYYILGLLGLL.....PGQPPKVKSEFNSSYSLTGYV 230

Scoring table: BLOSUM62  
 Gapop 10.0 , Gapext 0.5

Searched: 1276540 seqs, 311283816 residues

Total number of hits satisfying chosen parameters: 1276540

Minimum DB seq length: 0  
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications\_AA:\*

- 1: /cgn2\_6/ptodata/2/pubpaa/US07\_PUBCOMB.pep:\*
- 2: /cgn2\_6/ptodata/2/pubpaa/PCT\_NEW\_PUB.pep:\*
- 3: /cgn2\_6/ptodata/2/pubpaa/US06\_NEW\_PUB.pep:\*
- 4: /cgn2\_6/ptodata/2/pubpaa/US06\_PUBCOMB.pep:\*
- 5: /cgn2\_6/ptodata/2/pubpaa/US07\_NEW\_PUB.pep:\*
- 6: /cgn2\_6/ptodata/2/pubpaa/PCTUS\_PUBCOMB.pep:\*
- 7: /cgn2\_6/ptodata/2/pubpaa/US08\_NEW\_PUB.pep:\*
- 8: /cgn2\_6/ptodata/2/pubpaa/US08\_PUBCOMB.pep:\*
- 9: /cgn2\_6/ptodata/2/pubpaa/US09A\_PUBCOMB.pep:\*
- 10: /cgn2\_6/ptodata/2/pubpaa/US09B\_PUBCOMB.pep:\*
- 11: /cgn2\_6/ptodata/2/pubpaa/US09C\_PUBCOMB.pep:\*
- 12: /cgn2\_6/ptodata/2/pubpaa/US09\_NEW\_PUB.pep:\*
- 13: /cgn2\_6/ptodata/2/pubpaa/US10A\_PUBCOMB.pep:\*
- 14: /cgn2\_6/ptodata/2/pubpaa/US10B\_PUBCOMB.pep:\*
- 15: /cgn2\_6/ptodata/2/pubpaa/US10C\_PUBCOMB.pep:\*
- 16: /cgn2\_6/ptodata/2/pubpaa/US10\_NEW\_PUB.pep:\*
- 17: /cgn2\_6/ptodata/2/pubpaa/US60\_NEW\_PUB.pep:\*
- 18: /cgn2\_6/ptodata/2/pubpaa/US60\_PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	% Query		Length	DB	ID	Description
	Score	Match				
1	1174	100.0	230	9	US-09-998-598-2590	Sequence 2590, Ap
2	1174	100.0	230	10	US-09-888-257A-6	Sequence 6, Appli
3	1174	100.0	230	10	US-09-946-374-134	Sequence 134, App
4	1174	100.0	230	11	US-09-833-245-1256	Sequence 1256, Ap
5	1174	100.0	230	12	US-10-147-493-492	Sequence 492, App
6	1174	100.0	230	12	US-10-145-127-492	Sequence 492, App
7	1174	100.0	230	12	US-10-160-503-492	Sequence 492, App
8	1174	100.0	230	12	US-10-143-118-492	Sequence 492, App
9	1174	100.0	230	12	US-10-144-993-492	Sequence 492, App
10	1174	100.0	230	12	US-10-158-787-492	Sequence 492, App
11	1174	100.0	230	12	US-10-081-056-192	Sequence 192, App
12	1174	100.0	230	12	US-10-063-745-80	Sequence 80, Appl
13	1174	100.0	230	12	US-10-140-024-492	Sequence 492, App
14	1174	100.0	230	12	US-10-063-512-80	Sequence 80, Appl
15	1174	100.0	230	12	US-10-063-513-80	Sequence 80, Appl
16	1174	100.0	230	12	US-10-063-515-80	Sequence 80, Appl
17	1174	100.0	230	12	US-10-063-549-80	Sequence 80, Appl
18	1174	100.0	230	12	US-10-063-569-80	Sequence 80, Appl
19	1174	100.0	230	12	US-10-063-551-80	Sequence 80, Appl
20	1174	100.0	230	12	US-10-140-808-492	Sequence 492, App
21	1174	100.0	230	12	US-10-006-485A-134	Sequence 134, App
22	1174	100.0	230	12	US-10-013-907A-134	Sequence 134, App
23	1174	100.0	230	12	US-10-015-499A-134	Sequence 134, App

Run on: July 6, 2004, 13:55:23 ; Search time 73.2154 Seconds  
 (without alignments)  
 887.599 Million cell updates/sec

Title: US-10-063-588-80  
 Perfect score: 1174  
 Sequence: 1 MASLGLQLVGYYILGLLGLLG.....PGQPPKVKSEFNSSYSLTGYV 230

Scoring table: BLOSUM62  
 Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0  
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
 Maximum Match 100%  
 Listing first 45 summaries

Database : A\_Geneseq\_29Jan04:\*  
 1: geneseqp1980s:\*  
 2: geneseqp1990s:\*  
 3: geneseqp2000s:\*  
 4: geneseqp2001s:\*  
 5: geneseqp2002s:\*  
 6: geneseqp2003as:\*  
 7: geneseqp2003bs:\*  
 8: geneseqp2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result	%					Description
	No.	Score	Query Match Length DB	ID		
1	1174	100.0	230	2	AAAY36181	Aay36181 Human sec
2	1174	100.0	230	3	AAAY84609	Aay84609 A human m
3	1174	100.0	230	3	AAAY99378	Aay99378 Human PRO
4	1174	100.0	230	4	AAB66127	Aab66127 Protein o
5	1174	100.0	230	4	AAE04207	Aae04207 Human gen
6	1174	100.0	230	4	AAU12417	Aau12417 Human PRO
7	1174	100.0	230	4	AAU09178	Aau09178 Human PRO
8	1174	100.0	230	4	AAB87565	Aab87565 Human PRO
9	1174	100.0	230	4	AAB88342	Aab88342 Human mem
10	1174	100.0	230	5	ABP67991	Abp67991 Human col
11	1174	100.0	230	5	ABG95890	Abg95890 Human sec
12	1174	100.0	230	5	ABB84912	Abb84912 Human PRO
13	1174	100.0	230	5	AAU76534	Aau76534 Tumour-as
14	1174	100.0	230	5	ABG64507	Abg64507 Human alb
15	1174	100.0	230	5	ABB04707	Abb04707 Human SP8
16	1174	100.0	230	5	ABB95518	Abb95518 Human ang

17	1174	100.0	230	6	ABO17861	Abo17861	Novel	hum
18	1174	100.0	230	6	ABU81115	Abu81115	Human	PRO
19	1174	100.0	230	6	ABU90915	Abu90915	Novel	hum
20	1174	100.0	230	6	ABO33974	Abo33974	Human	sec
21	1174	100.0	230	6	ABU71991	Abu71991	Novel	hum
22	1174	100.0	230	6	ABU66815	Abu66815	Human	PRO
23	1174	100.0	230	6	ABU71545	Abu71545	Human	sec
24	1174	100.0	230	6	ABR47946	Abr47946	Human	sec
25	1174	100.0	230	6	ABU59896	Abu59896	Novel	sec
26	1174	100.0	230	6	ABU72326	Abu72326	Human	PRO
27	1174	100.0	230	6	ABU90999	Abu90999	Human	PRO
28	1174	100.0	230	6	ABO27320	Abo27320	Human	sec
29	1174	100.0	230	6	ABO25086	Abo25086	Human	sec
30	1174	100.0	230	6	ABR00178	Abr00178	Human	gen
31	1174	100.0	230	6	ABU92515	Abu92515	Human	sec
32	1174	100.0	230	6	ABU81185	Abu81185	Human	sec
33	1174	100.0	230	6	ABO53299	Abo53299	Novel	hum
34	1174	100.0	230	6	ABU67091	Abu67091	Human	sec
35	1174	100.0	230	6	ABU98302	Abu98302	Novel	hum
36	1174	100.0	230	6	ABU89307	Abu89307	Novel	hum
37	1174	100.0	230	6	ABU82514	Abu82514	Novel	hum
38	1174	100.0	230	6	ABU96478	Abu96478	Human	PRO
39	1174	100.0	230	6	ABU72148	Abu72148	Human	PRO
40	1174	100.0	230	6	ADA46011	Ada46011	Novel	hum
41	1174	100.0	230	6	ADA76442	Ada76442	Human	PRO
42	1174	100.0	230	6	ADB17137	Adb17137	Human	tra
43	1174	100.0	230	6	ADA19092	Ada19092	Human	PRO
44	1174	100.0	230	6	ADA61715	Ada61715	Homo sapi	
45	1174	100.0	230	6	ADB19500	Adb19500	Novel	hum

# ALIGNMENTS

RESULT 1  
AAY36181



Run on: July 6, 2004, 13:55:23 ; Search time 73.2154 Seconds  
 (without alignments)  
 887.599 Million cell updates/sec

Title: US-10-063-588-80  
 Perfect score: 1174  
 Sequence: 1 MASLGLQLVGYYILGLLGLLG.....PGQPPKVKSEFNSTGYV 230

Scoring table: BLOSUM62  
 Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0  
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
 Maximum Match 100%  
 Listing first 45 summaries

Database : A\_Geneseq\_29Jan04:\*  
 1: geneseqp1980s:\*  
 2: geneseqp1990s:\*  
 3: geneseqp2000s:\*  
 4: geneseqp2001s:\*  
 5: geneseqp2002s:\*  
 6: geneseqp2003as:\*  
 7: geneseqp2003bs:\*  
 8: geneseqp2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	% Query	Match	Length	DB	ID		Description
1	1174	100.0		230	2	AAY36181		Aay36181 Human sec
2	1174	100.0		230	3	AAY84609		Aay84609 A human m
3	1174	100.0		230	3	AAY99378		Aay99378 Human PRO
4	1174	100.0		230	4	AAB66127		Aab66127 Protein o
5	1174	100.0		230	4	AAE04207		Aae04207 Human gen
6	1174	100.0		230	4	AAU12417		Aau12417 Human PRO
7	1174	100.0		230	4	AAU09178		Aau09178 Human PRO
8	1174	100.0		230	4	AAB87565		Aab87565 Human PRO
9	1174	100.0		230	4	AAB88342		Aab88342 Human mem
10	1174	100.0		230	5	ABP67991		Abp67991 Human col
11	1174	100.0		230	5	ABG95890		Abg95890 Human sec
12	1174	100.0		230	5	ABB84912		Abb84912 Human PRO
13	1174	100.0		230	5	AAU76534		Aau76534 Tumour-as
14	1174	100.0		230	5	ABG64507		Abg64507 Human alb
15	1174	100.0		230	5	ABB04707		Abb04707 Human SP8
16	1174	100.0		230	5	ABB95518		Abb95518 Human an

Run on: July 6, 2004, 10:17:26 ; Search time 6305 Seconds  
(without alignments)  
10139.722 Million cell updates/sec

Title: US-10-063-588-79  
Perfect score: 1475  
Sequence: 1 gagagaagtcagcctggcag.....ctgggacatttaaaaaaata 1475

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 3470272 seqs, 21671516995 residues

Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : GenEmbl:\*  
1: gb\_ba:\*  
2: gb\_htg:\*  
3: gb\_in:\*  
4: gb\_om:\*  
5: gb\_ov:\*  
6: gb\_pat:\*  
7: gb\_ph:\*  
8: gb\_pl:\*  
9: gb\_pr:\*  
10: gb\_ro:\*  
11: gb\_sts:\*  
12: gb\_sy:\*  
13: gb\_un:\*  
14: gb\_vi:\*  
15: em\_ba:\*  
16: em\_fun:\*  
17: em\_hum:\*  
18: em\_in:\*  
19: em\_mu:\*  
20: em\_om:\*  
21: em\_or:\*  
22: em\_ov:\*  
23: em\_pat:\*  
24: em\_ph:\*  
25: em\_pl:\*  
26: em\_ro:\*  
27: em\_sts:\*  
28: em\_un:\*  
29: em\_vi:\*  
30: em\_htg\_hum:\*  
31: em\_htg\_inv:\*  
32: em\_htg\_other:\*  
33: em\_htg\_mus:\*  
34: em\_htg\_pln:\*

35: em\_htg\_rod:\*  
 36: em\_htg\_mam:\*  
 37: em\_htg\_vrt:\*  
 38: em\_sy:\*  
 39: em\_htgo\_hum:\*  
 40: em\_htgo\_mus:\*  
 41: em\_htgo\_other:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	% Query		Length	DB	ID	Description
	Score	Match				
1	1475	100.0	1475	6	AX092348	AX092348 Sequence
2	1475	100.0	1475	6	AX299996	AX299996 Sequence
3	1475	100.0	1475	6	AX395213	AX395213 Sequence
4	1475	100.0	1475	6	AX454606	AX454606 Sequence
5	1475	100.0	1475	6	AX464358	AX464358 Sequence
6	1475	100.0	1475	6	AX491084	AX491084 Sequence
7	1475	100.0	1475	6	AX697065	AX697065 Sequence
8	1475	100.0	1475	9	AY358474	AY358474 Homo sapi
9	1475	100.0	2959	9	AK075405	AK075405 Homo sapi
10	1475	100.0	109465	9	AL158821	AL158821 Human DNA
11	1473.4	99.9	1506	9	BC014424	BC014424 Homo sapi
12	1473.4	99.9	1918	9	AF177340	AF177340 Homo sapi
13	1472	99.8	2742	6	BD237562	BD237562 Membrane-
14	1470.2	99.7	2863	6	AX136129	AX136129 Sequence
15						

Run on: July 6, 2004, 10:17:25 ; Search time 4776.8 Seconds  
(without alignments)  
9220.961 Million cell updates/sec

Title: US-10-063-588-79  
Perfect score: 1475  
Sequence: 1 gagagaagtcagcctggcag.....ctgggacatttaaaaaaata 1475

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : EST:\*

- 1: em\_estba:\*
- 2: em\_esthum:\*
- 3: em\_estin:\*
- 4: em\_estmu:\*
- 5: em\_estov:\*
- 6: em\_estpl:\*
- 7: em\_estro:\*
- 8: em\_htc:\*
- 9: gb\_est1:\*
- 10: gb\_est2:\*
- 11: gb\_htc:\*
- 12: gb\_est3:\*
- 13: gb\_est4:\*
- 14: gb\_est5:\*
- 15: em\_estfun:\*
- 16: em\_estom:\*
- 17: em\_gss\_hum:\*
- 18: em\_gss\_inv:\*
- 19: em\_gss\_pln:\*
- 20: em\_gss\_vrt:\*
- 21: em\_gss\_fun:\*
- 22: em\_gss\_mam:\*
- 23: em\_gss\_mus:\*
- 24: em\_gss\_pro:\*
- 25: em\_gss\_rod:\*
- 26: em\_gss\_phg:\*
- 27: em\_gss\_vrl:\*
- 28: gb\_gss1:\*
- 29: gb\_gss2:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

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	2	731	49.6	822	12 BG386074	BG386074 602455248
	3	693	47.0	693	29 AY400251	AY400251 Homo sapi
	4	689.8	46.8	945	10 BE513091	BE513091 601171545
	5	676.4	45.9	693	29 AY400252	AY400252 Pan trogl
	6	643	43.6	680	10 BE304667	BE304667 601105783
	7	637.4	43.2	728	12 BG325755	BG325755 602424466
	8	617	41.8	978	12 BG164062	BG164062 602341087
	9	614.4	41.7	786	28 BZ215522	BZ215522 CH230-416
	10	606	41.1	643	12 BG328625	BG328625 602427889
	11	582.2	39.5	589	13 BU071883	BU071883 im35d11.y
c	12	577	39.1	676	10 AW385836	AW385836 CM2-LT004
c	13	575.6	39.0	630	10 AW837727	AW837727 CM1-LT004
c	14	555.4	37.7	623	10 AW837724	AW837724 CM1-LT004
c	15	555	37.6	555	13 BU073403	BU073403 im35d11.x
	16	552.6	37.5	777		

Run on: July 6, 2004, 10:17:25 ; Search time 702.749 Seconds  
 (without alignments)  
 8916.548 Million cell updates/sec

Title: US-10-063-588-79  
 Perfect score: 1475  
 Sequence: 1 gagagaagtcagcctggcag.....ctgggacatttaaaaaaata 1475

Scoring table: IDENTITY\_NUC  
 Gapop 10.0 , Gapext 1.0

Searched: 3373863 seqs, 2124099041 residues

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0  
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
 Maximum Match 100%  
 Listing first 45 summaries

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 2: geneseqn1990s:\*  
 3: geneseqn2000s:\*  
 4: geneseqn2001as:\*  
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 6: geneseqn2002s:\*  
 7: geneseqn2003as:\*  
 8: geneseqn2003bs:\*  
 9: geneseqn2003cs:\*  
 10: geneseqn2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

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3	1475	100.0	1475	4	AAS21489	Aas21489 Human cDN	
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5	1475	100.0	1475	4	AAF92097	Aaf92097 Human PRO	
6	1475	100.0	1475	6	ABS74417	Abs74417 Human cDN	
7	1475	100.0	1475	6	ABL88167	Abl88167 Human PRO	
8	1475	100.0	1475	6	ABK11089	Abk11089 cDNA enco	
9	1475	100.0	1475	6	ABL95656	Abl95656 Human ang	
10	1475	100.0	1475	7	ACD24098	Acd24098 Novel hum	
11	1475	100.0	1475	7	ACA67239	Aca67239 cDNA enco	
12	1475	100.0	1475	7	ACA91203	Aca91203 Novel hum	
13	1475	100.0	1475	7	ACD81580	Acd81580 Human cDN	
14	1475	100.0	1475	7	ACA60402	Aca60402 Novel hum	

15	1475	100.0	1475	7	ACA03848	Aca03848	cDNA	enco
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17	1475	100.0	1475	7	ABX89386	Abx89386	DNA	encod
18	1475	100.0	1475	7	ACA64025	Aca64025	cDNA	enco
19	1475	100.0	1475	7	ACA91289	Aca91289	cDNA	enco
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21	1475	100.0	1475	7	ACD42040	Acd42040	Human	sec
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 VERSION AF177340.1 GI:10503979  
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 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 REFERENCE 1 (bases 1 to 1918)  
 AUTHORS Gu,J.R., Wan,D.F., Zhao,X.T., Zhou,X.M., Jiang,H.Q., Zhang,P.P.,  
 Qin,W.X., Huang,Y., Qiu,X.K., Qian,L.F., He,L.P., Li,H.N., Yu,Y.,  
 Yu,J. and Han,L.H.  
 TITLE Novel human cDNA clone with function of inhibiting cancer cell  
 growth  
 JOURNAL Unpublished  
 REFERENCE 2 (bases 1 to 1918)  
 AUTHORS Gu,J.R., Wan,D.F., Zhao,X.T., Zhou,X.M., Jiang,H.Q., Zhang,P.P.,  
 Qin,W.X., Huang,Y., Qiu,X.K., Qian,L.F., He,L.P., Li,H.N., Yu,Y.,  
 Yu,J. and Han,L.H.  
 TITLE Direct Submission  
 JOURNAL Submitted (06-AUG-1999) National Laboratory For Oncogenes & Related  
 Genes, Shanghai Cancer Institute, 25/Ln 2200 Xie Tu Road, Shanghai  
 200032, P.R. China  
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 /protein\_id="AAG17984.1"  
 /db\_xref="GI:10503980"  
 /translation="MASLGLQLVGYILGLLGLLGLTLVAMLLPSWKTSYVVGASIVTAV  
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 RCTVFCQESRAKDRVAVAGGVFFILGGLLGFI PVAWNLHGILRDFYSPLVPDSMKFEI  
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# ORIGIN

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 Matches 1474; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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 Qy 61 AGAGCTTCAGCCTGAAGACAAGGGAGCAGTCCCTGAAGACGCTTCTACTGAGAGGTCTGC 120  
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 Db 459 AGAGCTTCAGCCTGAAGACAAGGGAGCAGTCCCTGAAGACGCTTCTACTGAGAGGTCTGC 518  
 Qy 121 CATGGCCTCTCTTGGCCTCCAACTTGTGGGCTACATCCTAGGCCTTCTGGGGCTTTTGGG 180



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Db	579		CACACTGGTTGCCATGCTGCTCCCCAGCTGGAAAAACAAGTTCTTATGTCGGTGCCAGCAT	638
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Db	699		CATCACCAGTGACATCTATAGCACCTTCTGGGCCTGCCCGCTGACATCCAGGCTGC	758
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Db	759		CCAGGCCATGATGGTGACATCCAGTGCAATCTCCTCCCTGGCCTGCATTATCTCTGTGGT	818
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Db	1119		CCAACCTCTTGCCACAAGGAGCTCTCCAAGGCCTGGTCAACCTCCCAAAGTCAAGAGTGA	1178
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Db	1179		GTTCAATTCTACAGCCTGACAGGGTATGTGTGAAGAACAGGGGCCAGAGCTGGGGGGT	1238
Qy	841		GGCTGGGTCTGTGAAAAACAGTGGACAGCACCCCGAGGGCCACAGGTGAGGGACACTACC	900
Db	1239		GGCTGGGTCTGTGAAAAACAGTGGACAGCACCCCGAGGGCCACAGGTGAGGGACACTACC	1298
Qy	901		ACTGGATCGTGTGAGAAGGTGCTGCTGAGGATAGACTGACTTTGGCCATTGGATTGAGCA	960
Db	1299		ACTGGATCGTGTGAGAAGGTGCTGCTGAGGATAGACTGACTTTGGCCATTGGATTGAGCA	1358
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Db	1479	CTTGAAACCCCATTCCTTAAGCCAGGACTCAGAGGATCCCTTTGCCCTCTGGTTTACCT	1538
Qy	1141	GGGACTCCATCCCCAAACCCACTAATCACATCCCCTGACTGACCCTCTGTGATCAAAGA	1200
Db	1539	GGGACTCCATCCCCAAACCCACTAATCACATCCCCTGACTGACCCTCTGTGATCAAAGA	1598
Qy	1201	CCCTCTCTCTGGCTGAGGTTGGCTCTTAGCTCATTGCTGGGGATGGGAAGGAGAAGCAGT	1260
Db	1599	CCCTCTCTCTGGCTGAGGTTGGCTCTTAGCTCATTGCTGGGGATGGGAAGGAGAAGCAGT	1658
Qy	1261	GGCTTTTGTGGGCATTGCTCTAACCTACTTCTCAAGCTTCCCTCCAAAGAAACTGATTGG	1320
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 DT 16-OCT-2001 (Rel. 40, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 15-MAR-2004 (Rel. 43, Last annotation update)  
 DE Claudin-2 (UNQ705/PRO1356).  
 GN CLDN2.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
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 RC TISSUE=Epithelium;  
 RA Reinecker H.-C., Sakaguchi T., Golden H.M.;  
 RL Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.  
 RN [2]  
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 RA Gu J.R., Wan D.F., Zhao X.T., Zhou X.M., Jiang H.Q., Zhang P.P.,  
 RA Qin W.X., Huang Y., Qiu X.K., Qian L.F., He L.P., Li H.N., Yu Y.,  
 RA Yu J., Han L.H.;  
 RT "Novel human cDNA clone with function of inhibiting cancer cell  
 RT growth.";  
 RL Submitted (AUG-1999) to the EMBL/GenBank/DDBJ databases.  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=22887296; PubMed=12975309;  
 RA Clark H.F., Gurney A.L., Abaya E., Baker K. et al.  
 RT "The secreted protein discovery initiative (SPDI), a large-scale  
 RT effort to identify novel human secreted and transmembrane proteins: a  
 RT bioinformatics assessment.";  
 RL Genome Res. 13:2265-2270(2003).  
 RN [4]  
 RP SEQUENCE FROM N.A.  
 RA Heath P.;  
 RL Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases.  
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 RP SEQUENCE FROM N.A.  
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 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
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 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
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 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
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 RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,  
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;

RT "Generation and initial analysis of more than 15,000 full-length  
 RT human and mouse cDNA sequences.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 CC -!- FUNCTION: Component of tight junction (TJ) strands.  
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein.  
 CC -!- SIMILARITY: Belongs to the claudin family.  
 CC -----  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
 CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use by non-profit institutions as long as its content is in no way  
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 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 DR EMBL; AF250558; AAF98151.1; -.  
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 DR EMBL; AY358474; AAQ88838.1; -.  
 DR EMBL; AL158821; CAD23055.1; -.  
 DR EMBL; BC015252; AAH15252.1; -.  
 DR EMBL; BC014424; AAH14424.1; -.  
 DR Genew; HGNC:2041; CLDN2.  
 DR InterPro; IPR006187; Claudin.  
 DR InterPro; IPR005411; Claudin2.  
 DR InterPro; IPR006188; Claudin\_reg.  
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 DR PROSITE; PS01346; CLAUDIN; 1.  
 KW Tight junction; Transmembrane.  
 FT TRANSMEM 8 28 POTENTIAL.  
 FT TRANSMEM 82 102 POTENTIAL.  
 FT TRANSMEM 117 137 POTENTIAL.  
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[Nucleotide](#)
[Protein](#)
[Genome](#)
[Structure](#)
[PMC](#)
[Taxonomy](#)
[OMIM](#)
[Books](#)

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[Details](#)





Range: from  to  Features: ☐ SNP ☐ CDD ☒ MGC ☐ HPRD ☐ STS

☐ 1: [P57739](#) Reports Claudin-2 (UNQ705...[gi:12229749]

[BLink](#), [Domains](#),  
[Links](#)

LOCUS P57739 230 aa linear PRI 01-MAY-2005

DEFINITION Claudin-2 (UNQ705/PRO1356) (SP82).

ACCESSION P57739

VERSION P57739 GI:12229749

DBSOURCE swissprot: locus CLD2\_HUMAN, accession [P57739](#);  
class: standard.  
created: Oct 16, 2001.  
sequence updated: Oct 16, 2001.  
annotation updated: May 1, 2005.  
xrefs: [AF250558.1](#), [AAF98151.1](#), [AF177340.1](#), [AAG17984.1](#), [AY358474.1](#),  
[AAQ88838.1](#), [AK075371.1](#), [BAC11575.1](#), [AL158821.16](#), [CAD23055.1](#),  
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[AAH71747.1](#)  
xrefs (non-sequence databases): Ensembl<sup>ENSG00000165376</sup>,  
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InterProIPR005411, InterProIPR006188, InterProIPR004031,  
PfamPF00822, PRINTSPR01077, PRINTSPR01589, PROSITEPS01346

KEYWORDS Tight junction; Transmembrane.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Hominidae; Homo.

REFERENCE 1 (residues 1 to 230)

AUTHORS Sakaguchi,T., Gu,X., Golden,H.M., Suh,E., Rhoads,D.B. and  
Reinecker,H.C.

TITLE Cloning of the human claudin-2 5'-flanking region revealed a  
TATA-less promoter with conserved binding sites in mouse and human  
for caudal-related homeodomain proteins and hepatocyte nuclear  
factor-1alpha

JOURNAL J. Biol. Chem. 277 (24), 21361-21370 (2002)

PUBMED [11934881](#)

REMARK NUCLEOTIDE SEQUENCE.  
TISSUE=Colon epithelium

REFERENCE 2 (residues 1 to 230)

AUTHORS Gu,J.R., Wan,D.F., Zhao,X.T., Zhou,X.M., Jiang,H.Q., Zhang,P.P.,  
Qin,W.X., Huang,Y., Qiu,X.K., Qian,L.F., He,L.P., Li,H.N., Yu,Y.,  
Yu,J. and Han,L.H.

TITLE Direct Submission

JOURNAL Submitted (??-AUG-1999)

REMARK NUCLEOTIDE SEQUENCE.

REFERENCE 3 (residues 1 to 230)

AUTHORS Clark,H.F., Gurney,A.L., Abaya,E., Baker,K., Baldwin,D., Brush,J.,  
Chen,J., Chow,B., Chui,C., Crowley,C., Currell,B., Deuel,B.,  
Dowd,P., Eaton,D., Foster,J., Grimaldi,C., Gu,Q., Hass,P.E.,  
Heldens,S., Huang,A., Kim,H.S., Klimowski,L., Jin,Y., Johnson,S.,  
Lee,J., Lewis,L., Liao,D., Mark,M., Robbie,E., Sanchez,C.,  
Schoenfeld,J., Seshagiri,S., Simmons,L., Singh,J., Smith,V.,  
Stinson,J., Vagts,A., Vandlen,R., Watanabe,C., Wieand,D., Woods,K.,  
Xie,M.H., Yansura,D., Yi,S., Yu,G., Yuan,J., Zhang,M., Zhang,Z.,

	Goddard,A., Wood,W.I., Godowski,P. and Gray,A.
TITLE	The secreted protein discovery initiative (SPDI), a large-scale effort to identify novel human secreted and transmembrane proteins: a bioinformatics assessment
JOURNAL	Genome Res. 13 (10), 2265-2270 (2003)
PUBMED	<u>12975309</u>
REMARK	NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
REFERENCE	4 (residues 1 to 230)
AUTHORS	Ota,T., Suzuki,Y., Nishikawa,T., Otsuki,T., Sugiyama,T., Irie,R., Wakamatsu,A., Hayashi,K., Sato,H., Nagai,K., Kimura,K., Makita,H., Sekine,M., Obayashi,M., Nishi,T., Shibahara,T., Tanaka,T., Ishii,S., Yamamoto,J., Saito,K., Kawai,Y., Isono,Y., Nakamura,Y., Nagahari,K., Murakami,K., Yasuda,T., Iwayanagi,T., Wagatsuma,M., Shiratori,A., Sudo,H., Hosoiri,T., Kaku,Y., Kodaira,H., Kondo,H., Sugawara,M., Takahashi,M., Kanda,K., Yokoi,T., Furuya,T., Kikkawa,E., Omura,Y., Abe,K., Kamihara,K., Katsuta,N., Sato,K., Tanikawa,M., Yamazaki,M., Ninomiya,K., Ishibashi,T., Yamashita,H., Murakawa,K., Fujimori,K., Tanai,H., Kimata,M., Watanabe,M., Hiraoka,S., Chiba,Y., Ishida,S., Ono,Y., Takiguchi,S., Watanabe,S., Yosida,M., Hotuta,T., Kusano,J., Kanehori,K., Takahashi-Fujii,A., Hara,H., Tanase,T.O., Nomura,Y., Togiya,S., Komai,F., Hara,R., Takeuchi,K., Arita,M., Imose,N., Musashino,K., Yuuki,H., Oshima,A., Sasaki,N., Aotsuka,S., Yoshikawa,Y., Matsunawa,H., Ichihara,T., Shiohata,N., Sano,S., Moriya,S., Momiyama,H., Satoh,N., Takami,S., Terashima,Y., Suzuki,O., Nakagawa,S., Senoh,A., Mizoguchi,H., Goto,Y., Shimizu,F., Wakebe,H., Hishigaki,H., Watanabe,T., Sugiyama,A., Takemoto,M., Kawakami,B., Yamazaki,M., Watanabe,K., Kumagai,A., Itakura,S., Fukuzumi,Y., Fujimori,Y., Komiyama,M., Tashiro,H., Tanigami,A., Fujiwara,T., Ono,T., Yamada,K., Fujii,Y., Ozaki,K., Hirao,M., Ohmori,Y., Kawabata,A., Hikiji,T., Kobatake,N., Inagaki,H., Ikema,Y., Okamoto,S., Okitani,R., Kawakami,T., Noguchi,S., Itoh,T., Shigeta,K., Senba,T., Matsumura,K., Nakajima,Y., Mizuno,T., Morinaga,M., Sasaki,M., Togashi,T., Oyama,M., Hata,H., Watanabe,M., Komatsu,T., Mizushima-Sugano,J., Satoh,T., Shirai,Y., Takahashi,Y., Nakagawa,K., Okumura,K., Nagase,T., Nomura,N., Kikuchi,H., Masuho,Y., Yamashita,R., Nakai,K., Yada,T., Nakamura,Y., Ohara,O., Isogai,T. and Sugano,S.
TITLE	Complete sequencing and characterization of 21,243 full-length human cDNAs
JOURNAL	Nat. Genet. 36 (1), 40-45 (2004)
PUBMED	<u>14702039</u>
REMARK	NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
	TISSUE=Teratocarcinoma
REFERENCE	5 (residues 1 to 230)
AUTHORS	Ross,M.T., Grafham,D.V., Coffey,A.J., Scherer,S., McLay,K., Muzny,D., Platzer,M., Howell,G.R., Burrows,C., Bird,C.P., Frankish,A., Lovell,F.L., Howe,K.L., Ashurst,J.L., Fulton,R.S., Sudbrak,R., Wen,G., Jones,M.C., Hurler,M.E., Andrews,T.D., Scott,C.E., Searle,S., Ramser,J., Whittaker,A., Deadman,R., Carter,N.P., Hunt,S.E., Chen,R., Cree,A., Gunaratne,P., Havlak,P., Hodgson,A., Metzker,M.L., Richards,S., Scott,G., Steffen,D., Sodergren,E., Wheeler,D.A., Worley,K.C., Ainscough,R., Ambrose,K.D., Ansari-Lari,M.A., Aradhya,S., Ashwell,R.I., Babbage,A.K., Bagguley,C.L., Ballabio,A., Banerjee,R., Barker,G.E., Barlow,K.F., Barrett,I.P., Bates,K.N., Beare,D.M., Beasley,H., Beasley,O., Beck,A., Bethel,G., Blechschmidt,K., Brady,N., Bray-Allen,S., Bridgeman,A.M., Brown,A.J., Brown,M.J., Bonnin,D., Bruford,E.A., Buhay,C., Burch,P., Burford,D., Burgess,J., Burrill,W., Burton,J., Bye,J.M., Carder,C., Carrel,L., Chako,J., Chapman,J.C., Chavez,D., Chen,E., Chen,G., Chen,Y., Chen,Z., Chinault,C., Ciccodicola,A., Clark,S.Y., Clarke,G., Clee,C.M., Clegg,S., Clerc-Blankenburg,K., Clifford,K., Cobley,V., Cole,C.G., Conquer,J.S., Corby,N., Connor,R.E., David,R., Davies,J., Davis,C., Davis,J., Delgado,O., Deshazo,D., Dhami,P., Ding,Y., Dinh,H., Dodsworth,S., Draper,H., Dugan-Rocha,S., Dunham,A., Dunn,M., Durbin,K.J., Dutta,I., Eades,T., Ellwood,M., Emery-Cohen,A.,

Errington, H., Evans, K.L., Faulkner, L., Francis, F., Frankland, J., Fraser, A.E., Galgoczy, P., Gilbert, J., Gill, R., Glockner, G., Gregory, S.G., Gribble, S., Griffiths, C., Grocock, R., Gu, Y., Gwilliam, R., Hamilton, C., Hart, E.A., Hawes, A., Heath, P.D., Heitmann, K., Hennig, S., Hernandez, J., Hinzmann, B., Ho, S., Hoff, M., Howden, P.J., Huckle, E.J., Hume, J., Hunt, P.J., Hunt, A.R., Isherwood, J., Jacob, L., Johnson, D., Jones, S., de Jong, P.J., Joseph, S.S., Keenan, S., Kelly, S., Kershaw, J.K., Khan, Z., Kioschis, P., Klages, S., Knights, A.J., Kosiura, A., Kovar-Smith, C., Laird, G.K., Langford, C., Lawlor, S., Leversha, M., Lewis, L., Liu, W., Lloyd, C., Lloyd, D.M., Loulseged, H., Loveland, J.E., Lovell, J.D., Lozado, R., Lu, J., Lyne, R., Ma, J., Maheshwari, M., Matthews, L.H., McDowall, J., McLaren, S., McMurray, A., Meidl, P., Meitinger, T., Milne, S., Miner, G., Mistry, S.L., Morgan, M., Morris, S., Muller, I., Mullikin, J.C., Nguyen, N., Nordsiek, G., Nyakatura, G., O'Dell, C.N., Okwuonu, G., Palmer, S., Pandian, R., Parker, D., Parrish, J., Pasternak, S., Patel, D., Pearce, A.V., Pearson, D.M., Pelan, S.E., Perez, L., Porter, K.M., Ramsey, Y., Reichwald, K., Rhodes, S., Ridler, K.A., Schlessinger, D., Schueler, M.G., Sehra, H.K., Shaw-Smith, C., Shen, H., Sheridan, E.M., Shownkeen, R., Skuce, C.D., Smith, M.L., Sotheran, E.C., Steingruber, H.E., Steward, C.A., Storey, R., Swann, R.M., Swarbreck, D., Tabor, P.E., Taudien, S., Taylor, T., Teague, B., Thomas, K., Thorpe, A., Timms, K., Tracey, A., Trevanion, S., Tromans, A.C., d'Urso, M., Verduzco, D., Villasana, D., Waldron, L., Wall, M., Wang, Q., Warren, J., Warry, G.L., Wei, X., West, A., Whitehead, S.L., Whiteley, M.N., Wilkinson, J.E., Willey, D.L., Williams, G., Williams, L., Williamson, A., Williamson, H., Wilming, L., Woodmansey, R.L., Wray, P.W., Yen, J., Zhang, J., Zhou, J., Zoghbi, H., Zorilla, S., Buck, D., Reinhardt, R., Poustka, A., Rosenthal, A., Lehrach, H., Meindl, A., Minx, P.J., Hillier, L.W., Willard, H.F., Wilson, R.K., Waterston, R.H., Rice, C.M., Vaudin, M., Coulson, A., Nelson, D.L., Weinstock, G., Sulston, J.E., Durbin, R., Hubbard, T., Gibbs, R.A., Beck, S., Rogers, J. and Bentley, D.R.

TITLE	The DNA sequence of the human X chromosome
JOURNAL	Nature 434 (7031), 325-337 (2005)
PUBMED	<u>15772651</u>
REMARK	NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
REFERENCE	6 (residues 1 to 230)
AUTHORS	Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G., Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D., Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K., Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F., Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L., Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L., Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S., Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J., Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J., McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S., Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W., Villalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A., Fahey, J., Helton, E., Kettelman, M., Madan, A., Rodrigues, S., Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y., Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D., Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M., Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smailus, D.E., Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A.
CONSRMT	Mammalian Gene Collection Program Team
TITLE	Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences
JOURNAL	Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
PUBMED	<u>12477932</u>
REMARK	NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
	TISSUE=Colon, Kidney, and Skin
COMMENT	[FUNCTION] Plays a major role in tight junction-specific obliteration of the intercellular space, through

calcium-independent cell-adhesion activity (By similarity).  
 [SUBUNIT] Can form homo- and heteropolymers with other CLDN.  
 Homopolymers interact with CLDN3, but not CLDN1, homopolymers.  
 Directly interacts with TJP1/ZO-1, TJP2/ZO-2 and TJP3/ZO-3 (By  
 similarity).  
 [SUBCELLULAR LOCATION] Integral membrane protein. Tight junctions  
 (By similarity).  
 [SIMILARITY] Belongs to the claudin family.

FEATURES	Location/Qualifiers
source	1..230 /organism="Homo sapiens" /db_xref="taxon:9606"
<u>gene</u>	1..230 /gene="CLDN2"
<u>Protein</u>	1..230 /gene="CLDN2" /product="Claudin-2"
<u>Region</u>	1..7 /gene="CLDN2" /region_name="Domain" /note="Cytoplasmic (Potential)." /evidence=not_experimental
<u>Region</u>	8..28 /gene="CLDN2" /region_name="Transmembrane region" /note="Potential." /evidence=not_experimental
<u>Region</u>	29..81 /gene="CLDN2" /region_name="Domain" /note="Extracellular (Potential)." /evidence=not_experimental
<u>Region</u>	82..102 /gene="CLDN2" /region_name="Transmembrane region" /note="Potential." /evidence=not_experimental
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<u>Region</u>	138..162 /gene="CLDN2" /region_name="Domain" /note="Extracellular (Potential)." /evidence=not_experimental
<u>Region</u>	163..183 /gene="CLDN2" /region_name="Transmembrane region" /note="Potential." /evidence=not_experimental
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<u>Site</u>	229..230 /gene="CLDN2" /site_type="unclassified" /note="Interactions with TJP1, TJP2 and TJP3 (By



similarity)."  
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//

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Feb 9 2005 14:31:10

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Range: from  to  ☐ Reverse complemented strand Features: ☐ SNP ☐ CDD

☒ MGC ☐ HPRD ☐ STS

☐ 1: [NM\\_020384](#). Reports Homo sapiens clau...[gi:38455423]

[Links](#)

LOCUS NM\_020384 2959 bp mRNA linear PRI 23-APR-2005  
 DEFINITION Homo sapiens claudin 2 (CLDN2), mRNA.  
 ACCESSION NM\_020384  
 VERSION NM\_020384.2 GI:38455423  
 KEYWORDS .  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
 Hominidae; Homo.  
 REFERENCE 1 (bases 1 to 2959)  
 AUTHORS Mankertz,J., Hillenbrand,B., Tavalali,S., Huber,O., Fromm,M. and Schulzke,J.D.  
 TITLE Functional crosstalk between Wnt signaling and Cdx-related transcriptional activation in the regulation of the claudin-2 promoter activity  
 JOURNAL Biochem. Biophys. Res. Commun. 314 (4), 1001-1007 (2004)  
 PUBMED [14751232](#)  
 REMARK GeneRIF: role for the paracellular barrier function by opening pores for small cations  
 REFERENCE 2 (bases 1 to 2959)  
 AUTHORS Colegio,O.R., Van Itallie,C., Rahner,C. and Anderson,J.M.  
 TITLE Claudin extracellular domains determine paracellular charge selectivity and resistance but not tight junction fibril architecture  
 JOURNAL Am. J. Physiol., Cell Physiol. 284 (6), C1346-C1354 (2003)  
 PUBMED [12700140](#)  
 REMARK GeneRIF: Results support a model in which claudins 2 and 4 create paracellular channels and the first extracellular domain is sufficient to determine both paracellular charge selectivity and transepithelial electrical resistance.  
 REFERENCE 3 (bases 1 to 2959)  
 AUTHORS Gonzalez-Mariscal,L., Betanzos,A., Nava,P. and Jaramillo,B.E.  
 TITLE Tight junction proteins  
 JOURNAL Prog. Biophys. Mol. Biol. 81 (1), 1-44 (2003)  
 PUBMED [12475568](#)  
 REMARK Review article  
 REFERENCE 4 (bases 1 to 2959)  
 AUTHORS Tsukita,S. and Furuse,M.  
 TITLE Claudin-based barrier in simple and stratified cellular sheets  
 JOURNAL Curr. Opin. Cell Biol. 14 (5), 531-536 (2002)  
 PUBMED [12231346](#)  
 REMARK Review article  
 REFERENCE 5 (bases 1 to 2959)  
 AUTHORS Sakaguchi,T., Gu,X., Golden,H.M., Suh,E., Rhoads,D.B. and Reinecker,H.C.  
 TITLE Cloning of the human claudin-2 5'-flanking region revealed a TATA-less promoter with conserved binding sites in mouse and human for caudal-related homeodomain proteins and hepatocyte nuclear factor-1alpha  
 JOURNAL J. Biol. Chem. 277 (24), 21361-21370 (2002)

PUBMED [11934881](#)  
 REMARK GeneRIF: Cloning of the human claudin-2 5'-flanking region revealed a TATA-less promoter with conserved binding sites in mouse and human for caudal-related homeodomain proteins and hepatocyte nuclear factor-1alpha.

REFERENCE 6 (bases 1 to 2959)  
 AUTHORS Tsukita,S., Furuse,M. and Itoh,M.  
 TITLE Multifunctional strands in tight junctions  
 JOURNAL Nat. Rev. Mol. Cell Biol. 2 (4), 285-293 (2001)  
 PUBMED [11283726](#)  
 REMARK Review article

REFERENCE 7 (bases 1 to 2959)  
 AUTHORS Heiskala,M., Peterson,P.A. and Yang,Y.  
 TITLE The roles of claudin superfamily proteins in paracellular transport  
 JOURNAL Traffic 2 (2), 93-98 (2001)  
 PUBMED [11247307](#)  
 REMARK Review article

REFERENCE 8 (bases 1 to 2959)  
 AUTHORS Kniesel,U. and Wolburg,H.  
 TITLE Tight junctions of the blood-brain barrier  
 JOURNAL Cell. Mol. Neurobiol. 20 (1), 57-76 (2000)  
 PUBMED [10690502](#)  
 REMARK Review article

REFERENCE 9 (bases 1 to 2959)  
 AUTHORS Itoh,M., Furuse,M., Morita,K., Kubota,K., Saitou,M. and Tsukita,S.  
 TITLE Direct binding of three tight junction-associated MAGUKs, ZO-1, ZO-2, and ZO-3, with the COOH termini of claudins  
 JOURNAL J. Cell Biol. 147 (6), 1351-1363 (1999)  
 PUBMED [10601346](#)

REFERENCE 10 (bases 1 to 2959)  
 AUTHORS Morita,K., Furuse,M., Fujimoto,K. and Tsukita,S.  
 TITLE Claudin multigene family encoding four-transmembrane domain protein components of tight junction strands  
 JOURNAL Proc. Natl. Acad. Sci. U.S.A. 96 (2), 511-516 (1999)  
 PUBMED [9892664](#)

REFERENCE 11 (bases 1 to 2959)  
 AUTHORS Furuse,M., Fujita,K., Hiiragi,T., Fujimoto,K. and Tsukita,S.  
 TITLE Claudin-1 and -2: novel integral membrane proteins localizing at tight junctions with no sequence similarity to occludin  
 JOURNAL J. Cell Biol. 141 (7), 1539-1550 (1998)  
 PUBMED [9647647](#)

COMMENT VALIDATED REFSEQ: This record has undergone preliminary review of the sequence, but has not yet been subject to final review. The reference sequence was derived from [AK075405.1](#).  
 On Nov 20, 2003 this sequence version replaced [gi:9966780](#).

Summary: Members of the claudin protein family, such as CLDN2, are expressed in an organ-specific manner and regulate the tissue-specific physiologic properties of tight junctions (Sakaguchi et al., 2002).[supplied by OMIM].

FEATURES

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# ORIGIN

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2161  caaatgagat  caggcccccc  cagggtccac  ccacagagca  ctacagagcc  tctgaaagac
2221  catagcacca  agcagagccc  ttcagattcc  cccactgtcc  atcggaagat  gctccagagt
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2341  gatctgagtg  atagctgcac  tgctgcctgg  gattgcagct  gaggtgggag  tggagaatgg
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2641 aggccgtctc cccttagcca agtcctcctc aggcttggag aacttcctca gcgtcacctc  
2701 cttcattgag ctttctctga tcaactccatc cctctcctac ccctccctcc cccaaccctc  
2761 aatgtataaa ttgcttcttg atgcttagca ttcacaattt ttgattgatc gttatttgtg  
2821 tgtgtgtgtc cgatctcaca agtatattgt aaacccttcg gtgggtgggg gccatctct  
2881 agacctctct gtatccccc aactatctgt aacagtgccca ggcacacagt aggtgatcaa  
2941 taaacacttg ttgattgag

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[NCBI](#) | [NLM](#) | [NIH](#)

Feb 9 2005 14:31:10

LOCUS BE513091 945 bp mRNA linear EST 07-AUG-2000  
 DEFINITION 601171545F1 NIH\_MGC\_15 Homo sapiens cDNA clone IMAGE:3545171 5',  
 mRNA sequence.  
 ACCESSION BE513091  
 VERSION BE513091.1 GI:9720302  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 REFERENCE 1 (bases 1 to 945)  
 AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.  
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
 JOURNAL Unpublished (1999)  
 COMMENT Contact: Robert Strausberg, Ph.D.  
 Email: [cgapbs-r@mail.nih.gov](mailto:cgapbs-r@mail.nih.gov)  
 Tissue Procurement: ATCC  
 cDNA Library Preparation: Ling Hong/Rubin Laboratory  
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
 DNA Sequencing by: NIH Intramural Sequencing Center  
 Clone distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LLNL at: [image.llnl.gov](http://image.llnl.gov)  
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 EcoRI; cDNA made by oligo-dT priming. Directionally  
 cloned into EcoRI/XhoI sites using the following 5'  
 adaptor: GGCACGAG(G). Size-selected >500bp for average  
 insert size 1.8kb. Library constructed by Ling Hong in  
 the laboratory of Gerald M. Rubin (University of  
 California, Berkeley) using ZAP-cDNA synthesis kit  
 (Stratagene) and Superscript II RT (Life Technologies)"

#### ORIGIN

Query Match 46.8%; Score 689.8; DB 10; Length 945;  
 Best Local Similarity 94.1%; Pred. No. 7.9e-190;  
 Matches 761; Conservative 0; Mismatches 42; Indels 6; Gaps 4;

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Db      126 AGAGCTTCAGCCTGAAGACAAGGGAGCAGTCCCTGAAGACGCTTCTACTGAGAGGTCTGC 185
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ID AAB88342 standard; protein; 230 AA.  
 DT 23-MAY-2001 (first entry)  
 DE Human membrane or secretory protein clone PSEC0059.  
 XX  
 KW Human; secretory protein; membrane protein; vaccine; gene therapy;  
 KW rheumatoid arthritis; diabetes.  
 XX  
 OS Homo sapiens.  
 XX  
 PN EP1067182-A2.  
 XX  
 PD 10-JAN-2001.  
 XX  
 PF 07-JUL-2000; 2000EP-00114090.  
 XX  
 PR 08-JUL-1999; 99JP-00194179.  
 PR 11-JAN-2000; 2000JP-00118775.  
 PR 02-MAY-2000; 2000JP-00183766.  
 XX  
 PA (HELI-) HELIX RES INST.  
 XX  
 PI Ota T, Isogai T, Nishikawa T, Kawai Y, Sugiyama T, Hayashi K;  
 XX  
 DR WPI; 2001-093989/11.  
 DR N-PSDB; AAF93769.  
 XX  
 PT Nucleic acids encoding secretory proteins/membrane proteins, useful in  
 PT gene therapy or as candidate target molecules in drug development.  
 XX  
 PS Claim 1; SEQ ID NO 52; 609pp + Sequence Listing; English.  
 XX  
 CC This invention relates to nucleic acid sequences AAF93744 - AAF93916  
 CC which encode human secretory or membrane proteins represented by AAB88317  
 CC - AAB88419. Included in the invention are primers AAF93917 - AAF94295 and  
 CC AAF62232 - AAF62235 which are used to isolate the cDNA sequences of the  
 CC invention. The invention also includes methods for the production of  
 CC antibodies directed against the proteins, and cDNA sequences, which can  
 CC be used in vaccines. The polynucleotide sequences can be used in gene  
 CC therapy. The polynucleotide sequences and the proteins they encode may be  
 CC used in the prevention, treatment and diagnosis of diseases associated  
 CC with inappropriate secretory protein/membrane protein expression. The  
 CC nucleic acids and complementary sequences may also be used as DNA probes  
 CC in diagnostic assays (e.g. polymerase chain reactions (PCR)) to detect  
 CC and quantitate the presence of similar nucleic acid sequences in samples.  
 CC They may also be used to study the expression and function of secretory  
 CC proteins/membrane polypeptides and their role in metabolism. The  
 CC polypeptides may be used as antigens in the production of antibodies  
 CC against them and in assays to identify modulators (agonists and  
 CC antagonists) of expression and activity. The antibodies and antagonists  
 CC may also be used as therapeutic agents to down regulate expression and  
 CC activity. The antibodies may also be used as diagnostic agents for  
 CC detecting the presence of the polypeptides in samples (e.g. by enzyme  
 CC linked immunosorbant assay (ELISA). Examples of diseases which may be  
 CC treated include rheumatoid arthritis and diabetes  
 XX  
 SQ Sequence 230 AA;





LOCUS AX136129 2863 bp DNA linear PAT 30-MAY-2001  
 DEFINITION Sequence 51 from Patent EP1067182.  
 ACCESSION AX136129  
 VERSION AX136129.1 GI:14272537  
 KEYWORDS .  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 REFERENCE 1  
 AUTHORS Ota,T., Isogai,T., Nishikawa,T., Kawai,Y., Sugiyama,T. and  
 Hayashi,K.  
 TITLE Secretory protein or membrane protein  
 JOURNAL Patent: EP 1067182-A 51 10-JAN-2001;  
 Helix Research Institute (JP)

FEATURES Location/Qualifiers  
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# ORIGIN

Query Match 99.7%; Score 1470.2; DB 6; Length 2863;  
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 Matches 1472; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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 Qy 61 AGAGCTTCAGCCTGAAGACAAGGGAGCAGTCCCTGAAGACGCTTCTACTGAGAGGTCTGC 120  
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Db	770	CCTCTGCTTTTCTGCTCATCCCAGAGAAATCGCTCCAATACTACGATGCCTACCAAGC	829
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Db	1370	GGCTTTTGTGGGCATTGCTCTAACCTACTTCTCAAGCTTCCCTCCAAAGAAACTGATTGG	1429
Qy	1321	CCCTGGAACCTCCATCCCACTCTTGTATGACTCCACAGTGTCCAGACTAATTTGTGCAT	1380
Db	1430	CCCTGGAACCTCCATCCCACTCCTGTTATGACTCCACAGTGTCCAGACTAATTTGTGCAT	1489
Qy	1381	GAACTGAAATAAAAACCATCCTACGGTATCCAGGGAAACAGAAAGCAGGATGCAGGATGGGA	1440
Db	1490	GAACTGAAATAAAAACCATCCTACGGTATCCAGGGAAACAGAAAGCAGGATGCAGGATGGGA	1549
Qy	1441	GGACAGGAAGGCAGCCTGGGACATTTAAAAAAATA	1475
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